```
================================================================
Sequence Listing could not be accepted due to errors.
See attached Validation Report.
If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).
Reviewer: Keisha Douglas
Timestamp: [year=2009; month=1; day=22; hr=16; min=26; sec=44; ms=514; ]
================================================================



* * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
Reviewer Comments:
<210>   56

<211>   17752
<212>   DNA
<213>   Phaeodactylum tricornutum, Physcomitrella patens


<210>   71

<211>   17061
<212>   DNA
<213>   Phaeodactylum tricornutum, Physcomitrella patens, Caenorhabditis
elegans


 The above <213> responses for sequence id#'s 56 and 71 are both
invalid, only one organism response is allowed for this line.

<210>   100
<211>   25
<212>   DNA
<213>   unknown



<220>
<221>   misc_feature
<222>   (1)..(25)
<223>   ACtrau-5'


<210>   103
```

```
<211>   22

<212>   DNA

<213>   unknown


<220>

<221>   misc_feature

<222>   (1)..(22)

<223>   YES-HIS-5'
```

Please explain the above <223> responses for sequence id#s 100 and 103.
FYI, please do not use foreign language in U.S. applications. Please
correct the remaining sequences showing similar errors.

```
*********************************************************
```

Application No: 10552013   Version No: 2.0

Input Set:

Output Set:

Started: 2009-01-07 16:25:11.916
Finished: 2009-01-07 16:25:23.759
Elapsed: 0 hr(s) 0 min(s) 11 sec(s) 843 ms
Total Warnings: 109
Total Errors: 51
No. of SeqIDs Defined: 148
Actual SeqID Count: 148

Error code	Error Description
W 402	Undefined organism found in <213> in SEQ ID (1)
W 402	Undefined organism found in <213> in SEQ ID (2)
W 402	Undefined organism found in <213> in SEQ ID (16)
W 402	Undefined organism found in <213> in SEQ ID (17)
W 402	Undefined organism found in <213> in SEQ ID (18)
W 402	Undefined organism found in <213> in SEQ ID (19)
W 402	Undefined organism found in <213> in SEQ ID (28)
W 402	Undefined organism found in <213> in SEQ ID (29)
W 402	Undefined organism found in <213> in SEQ ID (30)
W 402	Undefined organism found in <213> in SEQ ID (31)
W 402	Undefined organism found in <213> in SEQ ID (32)
W 402	Undefined organism found in <213> in SEQ ID (33)
W 402	Undefined organism found in <213> in SEQ ID (36)
W 402	Undefined organism found in <213> in SEQ ID (37)
W 213	Artificial or Unknown found in <213> in SEQ ID (52)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (52)
W 213	Artificial or Unknown found in <213> in SEQ ID (53)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (53)
W 213	Artificial or Unknown found in <213> in SEQ ID (54)

```
              Input Set:


              Output Set:



           Started:  2009-01-07 16:25:11.916
          Finished:  2009-01-07 16:25:23.759
           Elapsed:  0 hr(s) 0 min(s) 11 sec(s) 843 ms
    Total Warnings:  109
      Total Errors:  51
No. of SeqIDs Defined:  148
 Actual SeqID Count:  148


Error code       Error Description


E   224       <220>,<223> section required as <213> has Artificial sequence or
              Unknown in SEQID (54)

W   213       Artificial or Unknown found in <213>  in SEQ ID (55)

E   224       <220>,<223> section required as <213> has Artificial sequence or
              Unknown in SEQID (55)

W   402       Undefined organism found in <213>  in SEQ ID (56)

W   402       Undefined organism found in <213>  in SEQ ID (57)

W   402       Undefined organism found in <213>  in SEQ ID (58)

W   402       Undefined organism found in <213>  in SEQ ID (59)

W   213       Artificial or Unknown found in <213>  in SEQ ID (60)

W   213       Artificial or Unknown found in <213>  in SEQ ID (61)

W   213       Artificial or Unknown found in <213>  in SEQ ID (62)

W   213       Artificial or Unknown found in <213>  in SEQ ID (63)

W   213       Artificial or Unknown found in <213>  in SEQ ID (64)

W   213       Artificial or Unknown found in <213>  in SEQ ID (65)

E   224       <220>,<223> section required as <213> has Artificial sequence or
              Unknown in SEQID (65)

W   213       Artificial or Unknown found in <213>  in SEQ ID (66)

W   213       Artificial or Unknown found in <213>  in SEQ ID (67)

W   213       Artificial or Unknown found in <213>  in SEQ ID (68)

W   402       Undefined organism found in <213>  in SEQ ID (71)

W   402       Undefined organism found in <213>  in SEQ ID (72)
                This error has occured more than 20 times, will not be displayed

W   213       Artificial or Unknown found in <213>  in SEQ ID (75)
```

```
              Input Set:


              Output Set:



           Started:   2009-01-07 16:25:11.916
          Finished:   2009-01-07 16:25:23.759
           Elapsed:   0 hr(s) 0 min(s) 11 sec(s) 843 ms
   Total Warnings:   109
     Total Errors:   51
No. of SeqIDs Defined:   148
 Actual SeqID Count:   148
```

Error code	Error Description
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (75)
W 213	Artificial or Unknown found in <213> in SEQ ID (76)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (76)
W 213	Artificial or Unknown found in <213> in SEQ ID (77)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (77)
W 213	Artificial or Unknown found in <213> in SEQ ID (78)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (78)
W 213	Artificial or Unknown found in <213> in SEQ ID (79)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (79)
W 213	Artificial or Unknown found in <213> in SEQ ID (80)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (80)
W 213	Artificial or Unknown found in <213> in SEQ ID (81) This error has occured more than 20 times, will not be displayed
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (81)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (82)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (83)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (84)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (85)

Input Set:

Output Set:

Started:	2009-01-07 16:25:11.916
Finished:	2009-01-07 16:25:23.759
Elapsed:	0 hr(s) 0 min(s) 11 sec(s) 843 ms
Total Warnings:	109
Total Errors:	51
No. of SeqIDs Defined:	148
Actual SeqID Count:	148

Error code	Error Description
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (86)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (87)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (88)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (89) This error has occured more than 20 times, will not be displayed

SEQUENCE LISTING

<110>   Renz, Andreas
        Sozer, Nursen
        Frentzen, Margit
        Bauer, Jorg
        Keith, Stobart
        Fraser, Thomas
        Lazarus, Colin M
        Qi, Baoxiu
        Abbadi, Amine
        Heinz, Ernst

<120>   NOVEL PLANT ACYLTRANSFERASES SPECIFIC FOR LONG-CHAINED, MULTIPLY
        UNSATURATED FATTY ACIDS

<130>   13478-00002-US

<140>   10552013
<141>   2005-09-30

<150>   PCT/EP2004/003224
<151>   2004-03-26

<150>   DE103 14 759.4
<151>   2003-03-31

<150>   DE103 48 996.7
<151>   2003-10-17

<160>   148

<170>   PatentIn version 3.3

<210>   1
<211>   1047
<212>   DNA
<213>   Thraustochytrium

<220>
<221>   CDS
<222>   (38)..(952)
<223>   LPAAT

<400>   1

gggcggtgtc cggccgttcg agcgcgtgga cgccaac atg agc gcg tgg acg agg   55
                                        Met Ser Ala Trp Thr Arg
                                         1   5
gcc aag acc gcc gtg ggc ctc ctg acg ctg gcg cct gcg cgg ata gtg   103
Ala Lys Thr Ala Val Gly Leu Leu Thr Leu Ala Pro Ala Arg Ile Val
             10   15   20
ttc ctc gtg act gtc ctg ggc acg tac ggg ctc acg gtc gcg gcc tgc   151
Phe Leu Val Thr Val Leu Gly Thr Tyr Gly Leu Thr Val Ala Ala Cys
         25   30   35
acg cga ctt ggc gtc ccg aaa agc ttc gtg ctg ggc ctg acg cgg tgc   199

```
                Thr Arg Leu Gly Val Pro Lys Ser Phe Val Leu Gly Leu Thr Arg Cys
                    40                  45                  50
gtc gcg cga ctc acg ctc tgg ggg ctt ggg ttc tac cac att gag gtc        247
Val Ala Arg Leu Thr Leu Trp Gly Leu Gly Phe Tyr His Ile Glu Val
55                  60                  65                  70
tct tgc gac gcc caa ggc ctt cgg gag tgg ccg cgc gtg att gtc gcg        295
Ser Cys Asp Ala Gln Gly Leu Arg Glu Trp Pro Arg Val Ile Val Ala
                    75                  80                  85
aac cac gtc tcg tac ctg gag atc ttg tac ttc atg tcg acc gtg cac        343
Asn His Val Ser Tyr Leu Glu Ile Leu Tyr Phe Met Ser Thr Val His
                    90                  95                  100
tgc ccg tct ttc gtc atg aag aag acc tgc ctc cga gtc ccg ctt gtc        391
Cys Pro Ser Phe Val Met Lys Lys Thr Cys Leu Arg Val Pro Leu Val
        105                 110                 115
ggc tac att gcc atg gag ctg ggc ggt gtg att gtg gac cgc gag ggc        439
Gly Tyr Ile Ala Met Glu Leu Gly Gly Val Ile Val Asp Arg Glu Gly
        120                 125                 130
ggc ggt caa agc gca tcg gcg atc att cgc gac cgc gtg cag gag cct        487
Gly Gly Gln Ser Ala Ser Ala Ile Ile Arg Asp Arg Val Gln Glu Pro
135                 140                 145                 150
cct cga gat tcg tcg agc gag aag cac cac gcg cag ccg ctt ctt gtg        535
Pro Arg Asp Ser Ser Ser Glu Lys His His Ala Gln Pro Leu Leu Val
                    155                 160                 165
ttc ccc gag ggg acc acc acc aat gga agc tgc ctg ctc caa ttc aag        583
Phe Pro Glu Gly Thr Thr Thr Asn Gly Ser Cys Leu Leu Gln Phe Lys
                    170                 175                 180
acg gga gcc ttt cgt cct ggg gct ccg gtg ctt ccg gtc gtg ctt gag        631
Thr Gly Ala Phe Arg Pro Gly Ala Pro Val Leu Pro Val Val Leu Glu
        185                 190                 195
ttt ccg att gac aaa gcg cgt ggt gac ttt tcc ccg gcg tac gaa tcg        679
Phe Pro Ile Asp Lys Ala Arg Gly Asp Phe Ser Pro Ala Tyr Glu Ser
        200                 205                 210
gtc cac acg cca gct cac ctc ctt cgc atg ctc gca caa tgg agg cac        727
Val His Thr Pro Ala His Leu Leu Arg Met Leu Ala Gln Trp Arg His
215                 220                 225                 230
cgg ctt cgg gtg cgc tat ctt cct ctg tat gag ccc tct gcg gct gag        775
Arg Leu Arg Val Arg Tyr Leu Pro Leu Tyr Glu Pro Ser Ala Ala Glu
                    235                 240                 245
aag gtt gat gca gac ctt tat gcg cgg aac gtg cgc gac gaa atg gcg        823
Lys Val Asp Ala Asp Leu Tyr Ala Arg Asn Val Arg Asp Glu Met Ala
                    250                 255                 260
cgc gcg ctc aag gta ccc act gtg gag cag tct tac cgc gac aag ctc        871
Arg Ala Leu Lys Val Pro Thr Val Glu Gln Ser Tyr Arg Asp Lys Leu
        265                 270                 275
gtc tac cac gcg gat ctc atg ccg cac tac cag aag gcc ggc ccc gga        919
Val Tyr His Ala Asp Leu Met Pro His Tyr Gln Lys Ala Gly Pro Gly
        280                 285                 290
gcg ctc tat ctg tac gtc cga cct gac ctc ttg tagcactcat gcgcgtccca      972
Ala Leu Tyr Leu Tyr Val Arg Pro Asp Leu Leu
295                 300                 305
agcggtccag caacgggaga ttaaacacg atttcttagc ctacaaaaaa aaaaaaaaaa      1032
aaaaaaaaaa aaaaa                                                       1047



<210>   2

<211>   305
```

<212> PRT

<213> Thraustochytrium

<400> 2

```
Met Ser Ala Trp Thr Arg Ala Lys Thr Ala Val Gly Leu Leu Thr Leu
1               5                   10                  15
Ala Pro Ala Arg Ile Val Phe Leu Val Thr Val Leu Gly Thr Tyr Gly
            20                  25                  30
Leu Thr Val Ala Ala Cys Thr Arg Leu Gly Val Pro Lys Ser Phe Val
            35                  40                  45
Leu Gly Leu Thr Arg Cys Val Ala Arg Leu Thr Leu Trp Gly Leu Gly
        50                  55                  60
Phe Tyr His Ile Glu Val Ser Cys Asp Ala Gln Gly Leu Arg Glu Trp
65                  70                  75                  80
Pro Arg Val Ile Val Ala Asn His Val Ser Tyr Leu Glu Ile Leu Tyr
            85                  90                  95
Phe Met Ser Thr Val His Cys Pro Ser Phe Val Met Lys Lys Thr Cys
            100                 105                 110
Leu Arg Val Pro Leu Val Gly Tyr Ile Ala Met Glu Leu Gly Gly Val
        115                 120                 125
Ile Val Asp Arg Glu Gly Gly Gln Ser Ala Ser Ala Ile Ile Arg
        130                 135                 140
Asp Arg Val Gln Glu Pro Pro Arg Asp Ser Ser Ser Glu Lys His His
145                 150                 155                 160
Ala Gln Pro Leu Leu Val Phe Pro Glu Gly Thr Thr Thr Asn Gly Ser
            165                 170                 175
Cys Leu Leu Gln Phe Lys Thr Gly Ala Phe Arg Pro Gly Ala Pro Val
            180                 185                 190
Leu Pro Val Val Leu Glu Phe Pro Ile Asp Lys Ala Arg Gly Asp Phe
        195                 200                 205
Ser Pro Ala Tyr Glu Ser Val His Thr Pro Ala His Leu Leu Arg Met
        210                 215                 220
Leu Ala Gln Trp Arg His Arg Leu Arg Val Arg Tyr Leu Pro Leu Tyr
225                 230                 235                 240
Glu Pro Ser Ala Ala Glu Lys Val Asp Ala Asp Leu Tyr Ala Arg Asn
            245                 250                 255
Val Arg Asp Glu Met Ala Arg Ala Leu Lys Val Pro Thr Val Glu Gln
            260                 265                 270
Ser Tyr Arg Asp Lys Leu Val Tyr His Ala Asp Leu Met Pro His Tyr
        275                 280                 285
Gln Lys Ala Gly Pro Gly Ala Leu Tyr Leu Tyr Val Arg Pro Asp Leu
        290                 295                 300
Leu
305
```

<210> 3
<211> 1701

<212> DNA

<213> Physcomitrella patens

<220>
<221> misc_feature

<223> LPAAT

<400> 3

```
ggcacgaggg aaattggctt tctatgtggc cgtacttatt cgaggaggtc aacgaaacaa      60
aggtatgtct tattaatgaa aatgtctcca cacatgtatg ttgtttaggt atattctgtc     120
aactgaaaac ttgtttttaat ttttttcttaa attgaaattc tgtgcctgaa agccaactct   180
aggtccatca taatgtagca atatgatcag aagcgctcaa atgtgtcgtg aaagtttgct     240
tttgcaattt tcttttgctg ttaacctatt gattatgttg gaaccacaat acagacgctg     300
cttcacttca ttcttatggc aatgaatgtc gtgatgattc cggttaattt catcctacag     360
ggatatggat gttgtaaagg tgattttttgc aggtgataaa gtacctaagg agaaccgtgt    420
gatggtcatg tgcaaccatc gtaccgaagt ggactggatg tacatttgga acttagcaat     480
tcggaaaggc aagattgggt actgcaagta tgcggtgaag aactcagtga aaaacttacc     540
cttgtttggt tgggcatttt acgttttttga gtttctgatg ctgcatagaa agtgggaagt    600
ggatgctccc gtcatcaaga catacattga cagttttcaa gataaaagag atcctctctg     660
gctagtcgtg tttcctgaag cacagatttt tcgtaaggc tgaagtaccc atccatggct      720
ttgatgtata tctgcaatct tctctataat ctgcatttat tctctgttgt ttctctagca     780
agtaaatcat acttgcttaa tgtacttagc aatttgtcat ttttgactta ttgtgatgta     840
aatgtgattg actactatga cagtgaagcg aaacgggaca cgggcaatgc aattggaaga     900
gagaaaggct atccggagct tgtcaatgtg cttcaacctc gcactcgtgg ctttgtgact     960
tgcctttctc aatcgcgctg ctctttggat gcagtttatg acctcactat agggtacaag    1020
aagcggtgtc ccttgttcat caacaatgta ttcggaaccg atccatcgga agtgcacatt    1080
cacattcgcc gaataccaat ttctgagatt cctcaatcag aagacggtat gacgcagtgg    1140
ctgtatgatc tattttatca aaaggaccag atgttggcca gttttagtaa gacaggctct    1200
ttccctgaca gtggaattga agagagccct ttgaacatag tggaaggtgt ttgcaatgtt    1260
gctctacacg tagtccttag cggttgggta ttctggtgct gtttcattc ggtttggttg     1320
aagctttatg tggctttcgc tagtttgctg ctcgcgttta gtacctattt tgattggaga    1380
cctaaaccgg tttactctag tctacgtact aaaagaaaaa tcgtgtaaaa taaattcgtt    1440
agttgtaatt ggtttgttta ttccgattcc aaagctgagt ttaaggtga ggctcctctt     1500
taagctgatt tttgctatta attggctgct cccttgtttg tctgccgtaa attggcttta    1560
atacggttgt cttctgctga tgaacctcag tgcttcaaga cgatgtggcc ttttagcctt    1620
ctcctttacc catcttgacc agatgccaaa ctcgcaataa agcagatcaa taggtcgtgc    1680
cccaaaaaaa aaaaaaaaaa a                                              1701
```

<210> 4

<211> 714
<212> DNA

<213> Physcomitrella patens

<220>
<221> CDS
<222> (1)..(714)
<223> LPAAT

<400> 4

```
atg gct ttg atg tat atc tgc aat ctt ctc tat aat ctg cat tta ttc      48
Met Ala Leu Met Tyr Ile Cys Asn Leu Leu Tyr Asn Leu His Leu Phe
1               5                   10                  15
tct gtt gtt tct cta gca agt aaa tca tac ttg ctt aat gta ctt agc      96
Ser Val Val Ser Leu Ala Ser Lys Ser Tyr Leu Leu Asn Val Leu Ser
            20                  25                  30
aat ttg tca ttt ttg act tat tgt gat gta aat gtg att gac tac tat     144
Asn Leu Ser Phe Leu Thr Tyr Cys Asp Val Asn Val Ile Asp Tyr Tyr
```

```
              35                    40                        45
gac agt gaa gcg aaa cgg gac acg ggc aat gca att gga aga gag aaa          192
Asp Ser Glu Ala Lys Arg Asp Thr Gly Asn Ala Ile Gly Arg Glu Lys
      50                    55                    60
ggc tat ccg gag ctt gtc aat gtg ctt caa cct cgc act cgt ggc ttt          240
Gly Tyr Pro Glu Leu Val Asn Val Leu Gln Pro Arg Thr Arg Gly Phe
65                    70                    75                    80
gtg act tgc ctt tct caa tcg cgc tgc tct ttg gat gca gtt tat gac          288
Val Thr Cys Leu Ser Gln Ser Arg Cys Ser Leu Asp Ala Val Tyr Asp
                      85                    90                    95
ctc act ata ggg tac aag aag cgg tgt ccc ttg ttc atc aac aat gta          336
Leu Thr Ile Gly Tyr Lys Lys Arg Cys Pro Leu Phe Ile Asn Asn Val
              100                   105                   110
ttc gga acc gat cca tcg gaa gtg cac att cac att cgc cga ata cca          384
Phe Gly Thr Asp Pro Ser Glu Val His Ile His Ile Arg Arg Ile Pro
          115                   120                   125
att tct gag att cct caa tca gaa gac ggt atg acg cag tgg ctg tat          432
Ile Ser Glu Ile Pro Gln Ser Glu Asp Gly Met Thr Gln Trp Leu Tyr
      130                   135                   140
gat cta ttt tat caa aag gac cag atg ttg gcc agt ttt agt aag aca          480
Asp Leu Phe Tyr Gln Lys Asp Gln Met Leu Ala Ser Phe Ser Lys Thr
145                   150                   155                   160
ggc tct ttc cct gac agt gga att gaa gag agc cct ttg aac ata gtg          528
Gly Ser Phe Pro Asp Ser Gly Ile Glu Glu Ser Pro Leu Asn Ile Val
                      165                   170                   175
gaa ggt gtt tgc aat gtt gct cta cac gta gtc ctt agc ggt tgg gta          576
Glu Gly Val Cys Asn Val Ala Leu His Val Val Leu Ser Gly Trp Val
              180                   185                   190
ttc tgg tgc ttg ttt cat tcg gtt tgg ttg aag ctt tat gtg gct ttc          624
Phe Trp Cys Leu Phe His Ser Val Trp Leu Lys Leu Tyr Val Ala Phe
          195                   200                   205
gct agt ttg ctg ctc gcg ttt agt acc tat ttt gat tgg aga cct aaa          672
Ala Ser Leu Leu Leu Ala Phe Ser Thr Tyr Phe Asp Trp Arg Pro Lys
      210                   215                   220
ccg gtt tac tct agt cta cgt act aaa aga aaa atc gtg taa              714
Pro Val Tyr Ser Ser Leu Arg Thr Lys Arg Lys Ile Val
225                   230                   235


<210>   5

<211>   237

<212>   PRT

<213>   Physcomitrella patens

<400>   5


Met Ala Leu Met Tyr Ile Cys Asn Leu Leu Tyr Asn Leu His Leu Phe
1                   5                   10                  15
Ser Val Val Ser Leu Ala Ser Lys Ser Tyr Leu Leu Asn Val Leu Ser
              20                  25                  30
Asn Leu Ser Phe Leu Thr Tyr Cys Asp Val Asn Val Ile Asp Tyr Tyr
          35                  40                  45
Asp Ser Glu Ala Lys Arg Asp Thr Gly Asn Ala Ile Gly Arg Glu Lys
      50                  55                  60
```

Gly Tyr Pro Glu Leu Val Asn Val Leu Gln Pro Arg Thr Arg Gly Phe
65   70   75   80

Val Thr Cys Leu Ser Gln Ser Arg Cys Ser Leu Asp Ala Val Tyr Asp
                 85   90   95

Leu Thr Ile Gly Tyr Lys Lys Arg Cys Pro Leu Phe Ile Asn Asn Val
                100   105   110

Phe Gly Thr Asp Pro Ser Glu Val His Ile His Ile Arg Arg Ile Pro
         115   120   125

Ile Ser Glu Ile Pro Gln Ser Glu Asp Gly Met Thr Gln Trp Leu Tyr
     130   135   140

Asp Leu Phe Tyr Gln Lys Asp Gln Met Leu Ala Ser Phe Ser Lys Thr
145   150   155   160

Gly Ser Phe Pro Asp Ser Gly Ile Glu Glu Ser Pro Leu Asn Ile Val
                165   170   175

Glu Gly Val Cys Asn Val Ala Leu His Val Val Leu Ser Gly Trp Val
                180   185   190

Phe Trp Cys Leu Phe His Ser Val Trp Leu Lys Leu Tyr Val Ala Phe
         195   200   205

Ala Ser Leu Leu Leu Ala Phe Ser Thr Tyr Phe Asp Trp Arg Pro Lys
     210   215   220

Pro Val Tyr Ser Ser Leu Arg Thr Lys Arg Lys Ile Val
225   230   235

<210> 6

<211> 507

<212> DNA

<213> Physcomitrella patens

<220>
<221> misc_feature
<223> LPAAT

<400> 6

accaggtcga gatgcccatt attggactgt ttttgcaagc tttgcaaata atacccgtgg   60
accggactga tgctcagtct aggcaccatg cggctggcaa cgttcggcga agggctgtgg   120
acaatatgtg gtcccacgtc atgttgttcc cggagggcac taccaccaat ggcagagcaa   180
taatcgcctt caaaacagga gcattttcgc ctggtctccc tgtgcagcca atggttatta   240
gataccctca caagtatgtc aacccctctt ggtgtgacca aggaggtccg ttggtcgttg   300
tgttgcagct gatgactcag ttcatcaacc acatggaggt tgaatatttg ccggtcatga   360
agccaactgt gagagagatg aaataccctc atgaattcgc aagtagagtt cgcagcgaga   420
tggctaaagc gttaggcatc gtgtgcacag aacacagctt tctggatatt aagctagcgc   480
tggctgcaga aaagctcaaa cagcctt   507

<210> 7

<211> 1566

<212> DNA
<213> Physcomitrella patens

<220>
<221> CDS
<222> (1)..(1566)

<223> LPAAT

<400> 7

```
atg gag agc aca gca gat gtc gga atg tcc gac gac gat cct atc ctt        48
Met Glu Ser Thr Ala Asp Val Gly Met Ser Asp Asp Asp Pro Ile Leu
1               5                   10                  15
ctc aac ggg ctc gaa acg cca cta ctg gct gaa ttt cct ctt ggc gaa        96
Leu Asn Gly Leu Glu Thr Pro Leu Leu Ala Glu Phe Pro Leu Gly Glu
                20                  25                  30
cgg cct aca ata ggg ccg gag gca cca gta aat ccc ttc cat gaa ccc       144
Arg Pro Thr Ile Gly Pro Glu Ala Pro Val Asn Pro Phe His Glu Pro
            35                  40                  45
gat ggt ggt tgg aag acc aac aac gag tgg aat tac ttt caa atg atg       192
Asp Gly Gly Trp Lys Thr Asn Asn Glu Trp Asn Tyr Phe Gln Met Met
        50                  55                  60
aaa tcc att ttg ctg att cca ctt ctt ctc gtt cgt cta gtg agc atg       240
Lys Ser Ile Leu Leu Ile Pro Leu Leu Leu Val Arg Leu Val Ser Met
65                  70                  75                  80
ata aca atc gta gca ttt gga tat gtg tgg atc agg att tgt ctg atc       288
Ile Thr Ile Val Ala Phe Gly Tyr Val Trp Ile Arg Ile Cys Leu Ile
                85                  90                  95
ggc gtc aca gat ccc ttg ttt aag
Gly Val Thr Asp Pro Leu Phe Lys
```